		Helix-1	Str-1	Str-2	Helix-2	Str-3		Helix-3	Str-4	Str-5 of CT-hairpin div	Helix-4	Str-5 of Helix-4 div Helix-5	of TodA/AID ADOREC	
Secondary Structure CDD_Hsap_263657(PDB:1MQ0)	21	S Q E A K Q S A Y C	6 V G A A L L T Q	3 I F K G C N I E N	4 L G I CAERTAI Q KAV S	E 6 A I A I A S	7 S P C G A	CRQVMREFGT	N W P V Y M T K P	TYIVMT	- TIEIX-4	Sti-5 of Fielix-4 div	0—	CDD/CDA
CDD_Bsub_80258(PDB:1JTK) PITG_10446_Pinf_301106304 bsd_Ater_143955286(PDB:2Z3J)	10 138 14	A L K A R D M A Y A A A R E A R S S R A	6 V G A A L L T K 4 I G A A V L T E	3 V Y R G C N I E N 3 I Y S A G A V E N	4 M C N C A E RT A L F K A V S 2 L V L C A E H A A V M K M L T 2 G G P C A E L V V L G T A A A F 4 G S L C S E R N A T G K A V S 4 G S R C S E R N A T A H A R S 4 G S L C S E R N A T A H A R S 4 G S L C S E R A A T A H A R S 4 G S L C S E R A A T A H A R S 4 G S L C S E R A A T A H A R S 4 G S L C S E R A A T A H A R S 4 G S L C S E R A A T A H A R S 4 R S L C S E R A A F V Q L C M S	SE 6 M L A V A A	6 S P C G A 7 F P C G S	C R Q V I S E L C T C R E L L A D C G - C R Q V L L D L H P	DFPVYLVNA: GIKAIVKDS:	ETEDTR			116 242 117	
bsr_Bcer_461652 LmiF36.5940 Lmai_157877766	17 418	ATEKITMLYE KEOPNTEESN	6 G A A I R T K T	2 I I SAVHIEA 17 GV TAVNYFI	4 V T V C A E A I A I G S A V S 4 G S R G S E O N A M G K I A S	N 6TIVAVR	1 4 S P C G M	CRELISDYAP	DCFVLIEMN:	1 K L V K T T			117 128 599	Blasticidin S-deaminase
MIĆPUN 103900 Msp. 226520855 Pmar PMAR005400 Pemar 239900952	397 75	V Q E M K K H R D V A N K L R E Y M E R	2 2 V L A V L C V R 1 1 9 V L S M L H V R	7 Y F R G V N L E V 7 F F E G I N G E V	4 G S L C S E R N A I G N A L A 4 G S L C S E R A A I A H A R S	S S 3 D D L S L C	1 6 K P C G A 4 W P C G A	CKEWIIKTAE	2 P G F K V L M F G 2 P N F R V L A F D	R C D D V Y T			592 211	
PITG_06599_Pinf_262111987 Ehux1000015290_Ehux	17 35	L E G R R D Q H F T A H R V R D E R V R	9	8	4 G A T C A E R A A M A Q L Q L 4 N S I C A E R A A F V Q L C M	L 6K <mark>I</mark> YIVS 1L 9A <mark>V</mark> YIAS	6 T P G T L 6 T P G A L	C R E F L L S S P L C R E F M M S S P L	3 STPFVSRAT 3 DTRIVMEGG	K C H P C V G R R L D L			131 150	PITG_06599
mafB19_Nmen_254805593 Psta_3456_Psta_283781223 HMPREF9348_01319_Ecol_309794139	4862	TPWDTTDHFR	2 O G T V A F V F T	3 K V F G V N S T A 2	SALFHGEAHSIMRAYE	K 7DITIYV	2 L T C G P	CQGALPDLMK	2 GLKSLTVNA 2 GIERLKIVT	BRVGEIS			193 500	2 MofP40
PA39016_004380000_Paer_313112489 Pput 2613 Pput 148547830	1476 1007 740	Q I I D R F R S L K F I K A W G E A M V	17GTVAYIEI 25VVTAEGRI	3 K I F G V N S S V 2 3 V F T D V N Q T A 3	4 V A Y H A E A H S L M R A F E 4 A D A H A E I G V I Q K A F N	EK 7EITMYV IE 6DMTMNV PO 5RIVTEG	2 Y T C P N 3 D V C G Y	G R G D I A A A A S	2 G I D K L I I Y S : 2 G L K S L T I Q A : 2 G A D V E Y R W A :	BKTYYWE			161 116 852	6
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NAEGRDRAFT_51788_Ngru_290981146 AT1G20230_Atha_15223802	707 609	E V E L L K K E M K E V D S I R N K M E	7 P G V T T I E I 7 P G C S W I Q V	6 F V S N D K N H P 4 6 L L A G D K S H P 4	7 W Y A H T E G K I I S D L Y D 2 L C R H S E K L A M A Y A F I 0 L W G H S E K L A V V F G L L	H 8 I A N N L - N 8 V I K N L -	R V C G D R I C G D	CHNATKYISK	4 K I I V R D A S - 4 E I F I R D T N -	R F H H F E			850 750	
PSPPH_2819_Psyr_71734831 HMPREF9057_00892_Asp320532150	274 602	A S Q A R A D L P Q A A R V K E Q L P A	5 V K T V S S N D 5 R K <mark>A</mark> V S S D R	2 T L S D W G N K K 3 3 A L S G W S K D R 3	6 F S S H A E K Q M S I A S P N 6 F A S H A E R Q M A L N A K W 2 F A C H A E K Q L S L L T D K 5 S A S H A E K Q M L V K Q K N	IH P <mark>L</mark> GVSK IP R <mark>IGV</mark> SK	P M C T D P M C P D	CQGWFRSLAQ	4 E Q T V A D P K - 4 D W Y V T D P D -	G T W I F R			398 727	DYW
AceceDRAFT_3276_Acel_303241425 BACDOR_01063_Bdor_212691568	200 205	A Y T R A T D I I K R A E D I A K L L P	4 K G <mark>C</mark> V A S N G 4 G R T V <mark>C</mark> S D G	2 T L S G F D G K T 4 2 T I S G Y S K K R 4	2	K - P <mark>IGI</mark> SK NE 1A <mark>FGV</mark> NK	PMCPN KICEC	CYEFIQKIAQ	4 V K I T T D P K - 4 T I F V T Q P I D	ETYIFS			328 339	
PITG_03529_Pinf_301117730 AN3871.2_Anid_67526827 BURPS668_1122_Bpse_126439023	62 338 2997	S S K A S I S F A K	4 M D K L L E G K	I K S G F G A F G 4	8 Y W C H A H K Q K L M D I K E	K 1 8 A I V V D K	A M C E D	GREENRRINO	4 CICIQDPE - 4 SIQLYERT -	O H Y ❖			213 585 314	
Daci 4514 Daci 160899946	3564 657	S S L G K I D Q L R	1 1 A FAEYNI -	3 I G E L V G I S G 2	4 R K V D S E A K I L N N I A A 5 R M M D S E V K I L E H L G G 3 R N I D G E Y K L L E T I A Q 9 R Q A D A E L K A L R N L E S	N 8LHLFSE	1 P P C E S 1 P L C I S 1 K A C Q S	CS G V V S Q F H E	3 NIKINVMDS 3 GIRVIVNHG 3 NIQLNIFT-	PKR*			368 795	9 BUDDSEER 1122
hrpS3_Nmen_224022381 PSPA7_3257_Paer_152987428 ywqJ_Bsub_16080672 LMHCC_1757_Lmon_217965034	67 466	P S N A A K K E L V L S R I K S S G L T	6 T T A R F E Y S 5 P A V A G V L D	9 R V Y N A M S G Q 4 5 Y Y F G I N N I D 3	9 R Q A D A E L K A L R N L E S 1 A G S H A E V N A L N E A L L	D11LTGFIS	1 A P C E S	CKPMLENVLP CEYITQNTNY	3 Y V S E A H V S -	YLPNAR			223	
EcolM 010100026429 Ecol 307224485	358 52	K F K N K L D M L R L L A K A T S N T Q	1 4 A V A D V R I E 5 R A V S A V V D	5 F L A H S K I H G 2 5 I Y Y G E S G W P 2	1 A G S H A E V N A L N E A L L 9 R Y N D T E A K I L E D I A S 2 I E N C A E F K A V N E A L K 4 S G I H G E V H G L N E L L W	Q 8QIDLYT	2 A T C Q S 9 P M C K N	CTNIILEFRR COISIFGAVV	3 NIKLNIFTE	•			491 164	YwqJ
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dcda_BPT4_58177055(PDB:1VQ2) MK0935_Mkan_20094371(PDB:3G8Q) ribD_Bsub_83754936(PDB:2B3Z)	11 19	T V L Q I A Y L V S D V K K I L N E I P	8 K V G A V I E K 3 V T A A L L E G	3 I I S T G Y N G S S 2 I V A V E E A D D	2 N E I H A E L N A I L F A A E E H A E R K L V R R H D - 1 G E A H A E V H A I H M A G A	N 7TMYVTL - 4VVFVTA	S P C P D R P C L Y	CAKAIAQSGI CARELAE <mark>A</mark> GV	1 K L V Y C E T Y D 1 G V V Y L G R G R		G L G P Y Y L A R	1 G I E V F N V P K 1 G V E V V E V H P	176 108	dCMP deaminase CDAT8
TAD1_Scer_6321194 ADAR_Hsap_70166852	25 842	EEISTRVINE	2 1 I L A G V A A I 1	10 I L S I A T G V K 1	1	V35ALYISR	EPCSH LPCGD6 APCGD6	3 C S D K L L M K Q R 1	9 Y I V I P N L E D		2 K H H L E Q S F H 1	1 G I E V K E G I L 2 Q A I	295	RibD Tad1
TAD3 Scer 9755339 CNBC2910 Cneo 134109371	173 434	LSVKMATAGK	3 M V S V F V D P	4 D K V V A E D G R	6	R 1 7 D V Y L T H	E P C S M	CSMALIHSRV	1 RV V F L T E M Q		8 5 G D G Y C M N D	6 T Y E A F Q W I G 2 Y P V	V G Q V D R D V C 321	Tad3
tadA_Aae_60593939(PDB:1WWR) TAD2 Scer 6322425	31 11	LREAKRAFEK	4 V G A I I V K E	2 I I S K A H N S V	5 P T A H A E M L A I K E A C R	R 9ELYVTL	E P C I M	CSYALVLSRI CASALKOLDI	1 K V I F S A L D K		4 V V S V F N I L D 2 N G T V L S V N H 1	6 R V K W E Y Y P L 1 E A 1	SELLSEFFK 164	Tad2/TadA
Bd3614_Bbac_42524957 MICPUN_102230_Msp255082492	161 253	P R G S V L H D Y D N T Q T Q L W E R D	3 A A F L L N D Q 3 V A A L V S P R	2 L <mark>L</mark> S Y G <mark>V</mark> N S N 2 V T D A A R N V N	3 K T L H A E V N L V Q R L H R 3 K C L H A E W N L L A P T L W 4 R G I H A E I F S I R K V E E	RE 9 V <mark>L</mark> Y S T H / G 3 O R V L <mark>V</mark> T L	K P C K M Q C C K M	C A G M I Y H W C E C A A L V C A A A D	5 KVYYSVEE - 8 EVVYLNPD -		2 G L S R Q T V L D 2 S L A R D T Q L R	6 H I S K 8 A A P C E	275 394	Bd3614
PmCDA1_Petma_126507754 APOBEC1_Hsap_2696116	19	EPWEFDVFYD	6 E A C L L Y E I	9 R S S G K N T T -	N#V=VNFIKKFTS	SE 9 SITWFL	2 S P C A D 2 S P C W E	C A E K I L E W Y N C S Q A I R E F L S	6 G H T L K I W A C 3 G V T L V I Y V A	1	2 G L W N L R D N - 2 G L R D L V N S -	G V G L N V M V S 1 H Y C G V T I Q I M R A 1 E Y	QCCRKIFIQMI 165 YHCWRNFVNII 158	
AICDA_Hsap_10190700 APOBEC2_Hsap_5802978(PDB:2NYT) APOBEC3G_Hsap_283807058(PDB:1IR2)	11 52 25	F L Y Q F K N V R W F K F Q F R N V E Y	7 Y L C Y V V K R 1	LOFGYLRNKN- LORGYLEDEH-	- G C H V E L L F L R Y I S D A A A H A E E A F F N T I L F 6 E G R H A E L C F L D V I P F	OW 8 R V T W F T	2 S P C Y D 2 S P C A A 2 S P C F S	CARHVADELR	3 NL SLRIFTA 3 NL RL LILVG	1	3 G L R R L H R A - 2 A L K K L K E A -	G C K L R I M K P 1 D F	FYCWNTFVELL 153 FYVWQNFVELK 193	AID/APOBEC
APOBEC4_Hsap_74751569 ZK287.1_Cele_17566846	48 149	FCQIF-GFPY	7 KHLTFYEL	4 G S L V Q K G H A	5 N Y I H P E S M L F E M N G Y G E P H V E E Q L V A A I Y D	L11HIILYS	2 S P C N E 2 S P C F H 1	4 CISKMYNFLI	3 GITLSIYFS	1	7 A L R S L A S L -	W PRV V L S P I 3 I W	HSVLHSFISIT 203	
Tsp_00370_Tspi_339240643 NEMVEDRAFT_v1g248558_Nvec_156208551	100 1 57	P S H P D Q H T P N D K V I G N K K F F	16VMVAKLVS	5 TADYFVAET 8 KSVRRYTNC	2 P R Q H V E Q I F Y A E L I N 2 K M K H A E E F F L M D I D C	A 1 0 Q I C L F M	2 S P C F H 1 2 O P C H L 1	8 CAETLAIAYK	9 D L Q M T V K F L 4 N V F T V T K P T	1	3 G I L C M L Q A -	GISVEPLSR1DW	YALVESDDQQR 278	AID/APOBEC
MICPUN_56782_Msp255074389 B3qp45 Wend_222825157	41 2136	N S L L G G V A Q L	4 0 V A A L R D R	3 R F L S R Y S N C	1 L S S H A E E Y V V R D E E L	. V 2 3 T L T L Y Q	2 Q P C H G 1 2 S P C Q N	0 C S D A L V A G L H C T R E I I E Y V K	7 G V S L R V A V S 7 N F K L S L G M E	3	0 G I R V F A A A A 3 G S M E Q A R R I	2 G V T L E A L N A 1 D W A 1 A T S L A A M K V 4 A L I	A F L V S L C D N G - 260 N L K Y A R M Y E N V 228	1 -like
PSEBR_m1207_Pbra_330810772 OTT_1508_Otsu_189184415	224	- M F L A K F E E Y E L I S D H N L I H	2	3 V P R H P K L 7 L Y V I K N N S S	- NEHTEQQIFTYIVS 2 EQQHAEMVVLEYVHN 2 NQIHAEMILLEHIHS 2 NKGHAEMRIVDYLRK	F14E <mark>I</mark> Q <mark>I</mark> IS IK 7GNV <mark>Y</mark> IG	2 S P C T D 3 L S C F T	C A K K L A E L P E C Q K V I E Y Y N N	8 D S S Q A T Y S I 1 E S N V K L E N H	2 1	2 S I K T M T S A - 7 D V V S V D D L I 1	K <mark>WKI</mark> EAV DE: .1ISAFPFGK-	IPS <mark>L</mark> MLKPADM 168 378	
OTT_1656_Otsu_189184563 A1I_04250_Rbel_157827168	138 68	V L G K N Y R L I N A F R A K Q D L M K	17RV <mark>CSYF</mark> KD 17AI <mark>I</mark> KE <mark>F</mark> EK	7 L I I I Q N H S T 4 T L V Y D G P	2 N Q I H A E M I L L E H I H S 2 N K G H A E M R I V D Y L R K	SD 6 SEA Y I G R 9 E N I Y I G	3 L S C M P 3 L C C T S	C S K V I K L Y N E C D V A I N K S N L 1	1 A N N L D V E Y H 0 E H K V N I D P T :	1 1	7 SIVSEEHFV 7 DEVKLEAFL 1	7 S	287 230	
Namu 1026 Nmul 258651268 Aasi 0969 CAmo 189502339 XCV4233 Xcam 78049789	391 373 59	L R G A L D P G A R V T D R L H K I D R	1 6 L Q S G D Y R A 1 1 3 G V F G A F	T E Q I S G	3	D11IVRDLG	3 L A C G A 3 R P C A C 3 P C C F D	C K L A F E A Y N Q C F I Y M I L K G L	6 Q H N G A L W N S	1	7 NHEAALAYV 7 QELLEVVNR 1	4 P E G <mark>Y</mark> L D D R - . 1 E G <mark>K</mark> E I Y D F -	556	
Acid345_T142_CKor_94968171 TRIADDRAFT_55868_Tadh_196003532	790 433	IGGKDPRAAQ	1 8 S S G F V I Q P	8 V V A W N S G D P	4 N I S H A E R Q F I D W F R G	Q 9SVEVEV	3 D I C T N 3 L S C P O	CESDISDLKR	1 Y D K V K F K W D	1	4 X 6 T K *	2 E P D V D T T E -	923	
TRIADDRAFT 59614 Tadh 196011375 SELMODRAFT 427619 Smoe 302814633	451 88	DEKSQILFDV	14ISYCRLSP	SLSVISFEI-	2 E G F H A E I C I P E M C S K 4 D D L H A E M Q L I D Y E S -	- 2 P P K R I A	3 L H C P M 3 L P C F L	CYLAIWAKNK	8 SYKSDVIL-	1	1 W N W P K S F L N	2 L L V F L F L G -	585 241	OTT_1508
LmjF33.1760 Lmaj 157875062 NCU05870 Ncra_85094315	130 231	L T Q E S L Q A A V S R L O S Y N I A V	3 G V A G V F Q I 1 5 D F E V V P V P 1	2 F V L V T G E L 7 I K R F P D K 3	G S V H C E Q K L P K G C H A E K K L L E H L E T 2 P Y V H A E L V L L D S I L R 2 L A V H S E V L L H H W L L T	Q 1 5 K A L I V G	2 L P C V A 3 P T C R L	CRLFAIAFES CKLYIDNHP-	1 A V L L P S H G - S G V E F R H G -	2	O K T K D I N A M L 1 7 R O D I H N K M L 1	. 2 P K H R R L L R - . 3 N V A E R K L H -	271 437	
NCU05062_Ncra_85079856 MGG_12698_Mory_145610470	247 559	Q R I R A Y R A S V K T V R S A L K I I	1	L 9 V G R M T <mark>S</mark> N 3 L 6 G <u>R</u> Y Y G <mark>V</mark> C 3	2	D 1 3 S W P Y I G LQ 4 W P R A M G	3 P T C K L 3 S A C F L	C	S G V E V R A S - - H F S V S A C -	2	4 RQIMLDRIL1 4 ASAILRICD	. 3 K S P <mark>L</mark> S Y K H - 8 P G A R V C P P -	452 755	
CC1G 10109 Ccin 299756773 TGME49 092320 Tgon 237838551	269 357	I I R W I N K L C S V C D L A G F A L H	2 4 L D I E V Y H Q 2 3 1 L A R V G V G S 2	2 2 Y L R G K F D S S 3 2 1 H I V T A P S E - 5	9 L P V H A E V Q L T M H Y L A 0 R S V H C E V F L L R R V Q T 3 M I R H A E T L L Q E 2 - C A H G E L T A L W N A I A	A 3 I L P Y I G	3 L S C V P 7 G C C S A	G S V Y F E H L A D G R Q M D A R S F	3 D S V S T R G S - F L V H G E Q K D	2	1 D K R M E E L H D 9 V G Q R L A A V L	8 L L W R Y I D E - 7 F V S G V S V G -	471 619	
XOO 2897_Xory_84624554 SC4A7.11_Scoe_21220850 BURPS668_A2951_Bpse_126445357	1382 1412	A Q S Q D D G G I N K L T A R A S T A V	1 - GCPVGLV1	P V F G N S K L R I 1 L O A Y R Y R T E S E 3	2 - C A H G E L T A L W N A I A 0 F S G H S E T E I L G K L E A - K S H S E D A I I D F I K G 9 G G N H A E R V L M G L	A - 71 VEMYI A - 71 TALYT	2 S P C S K 2 Q P C P A 2 S P C A E	CASVLTGSLK	1 G T P V T W S V P		8 K V A A K H L C A ; 9 R S L L D S Y V R	G T E V F W P K P K P K P K P K P K P K P K P K P	152 153 153	6 XOO_2897
sce4086_Scel_162452362 consensus/65%	1234	PLGLIVLQQV	4 H P L F G A V S 1	15 VAAVLLDDG	9 G G N H A E R V L M G L	- 7 V V A V Y T	2 S P C T G . S C	GHDLLDSSLG Cp.hl.h	1 DVPVYYTHE	n h	3 E A D R N Q F C R	GG* . hph ch	h h n . h . n .	7